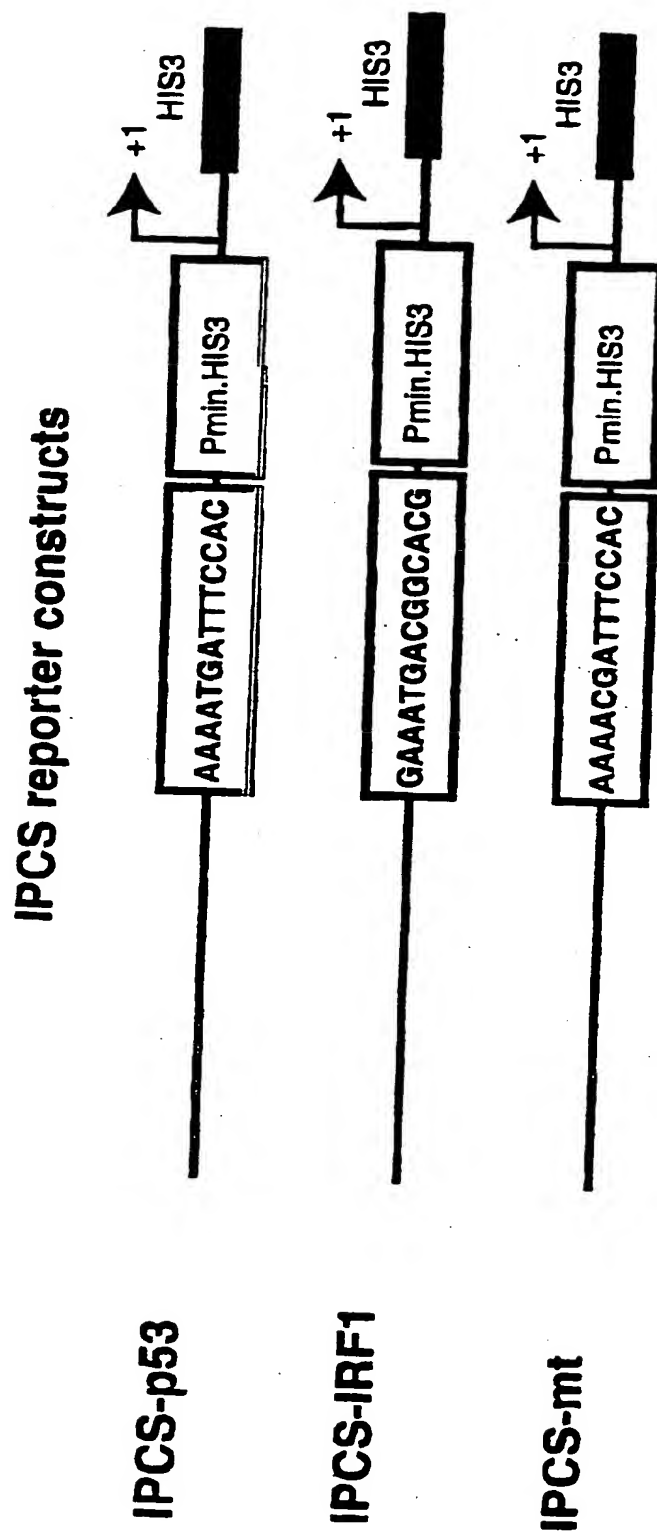
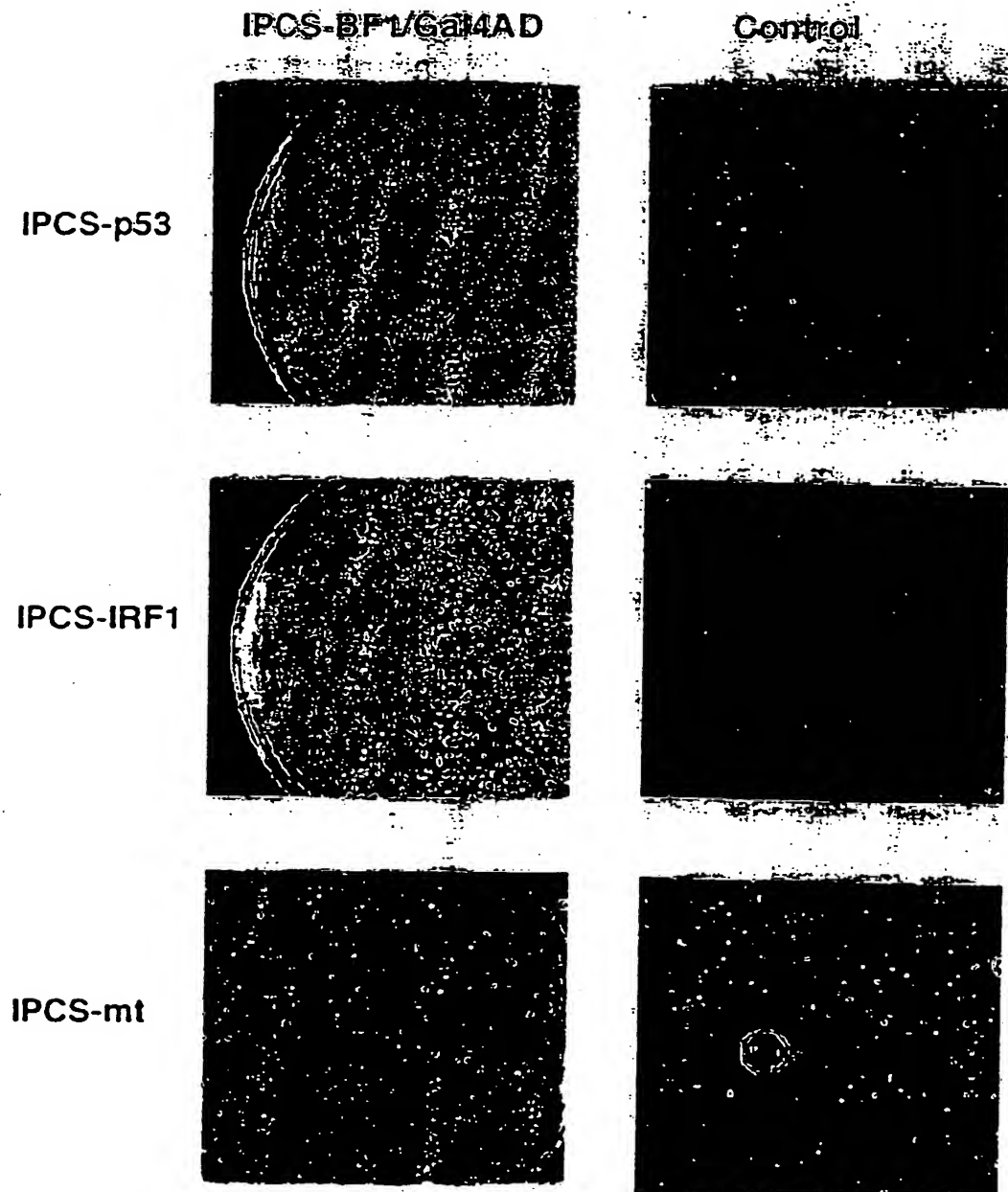


Figure 1A

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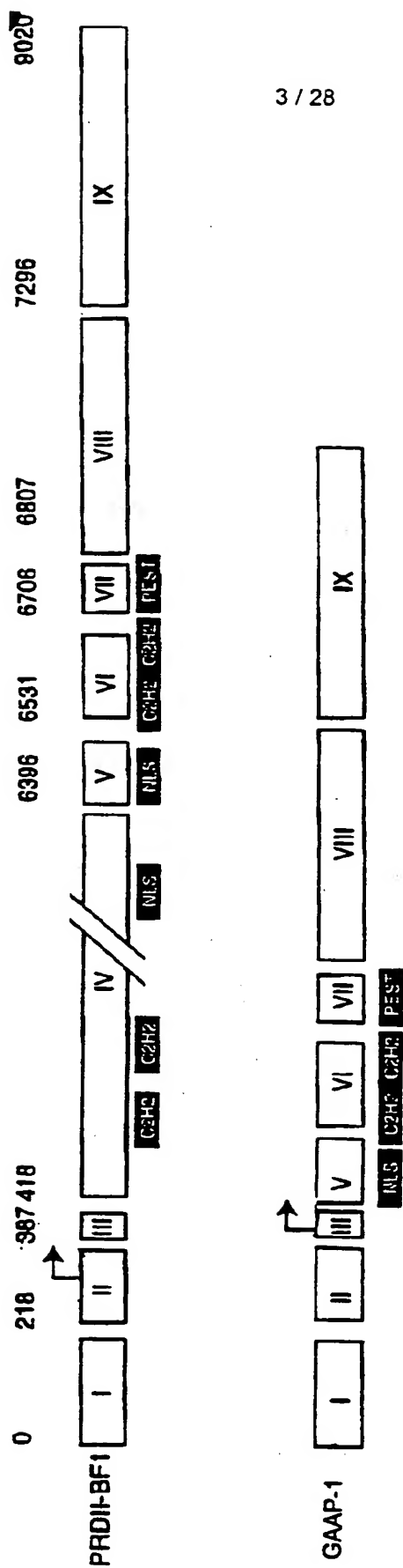
Figure 1B



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11. 10. 2002

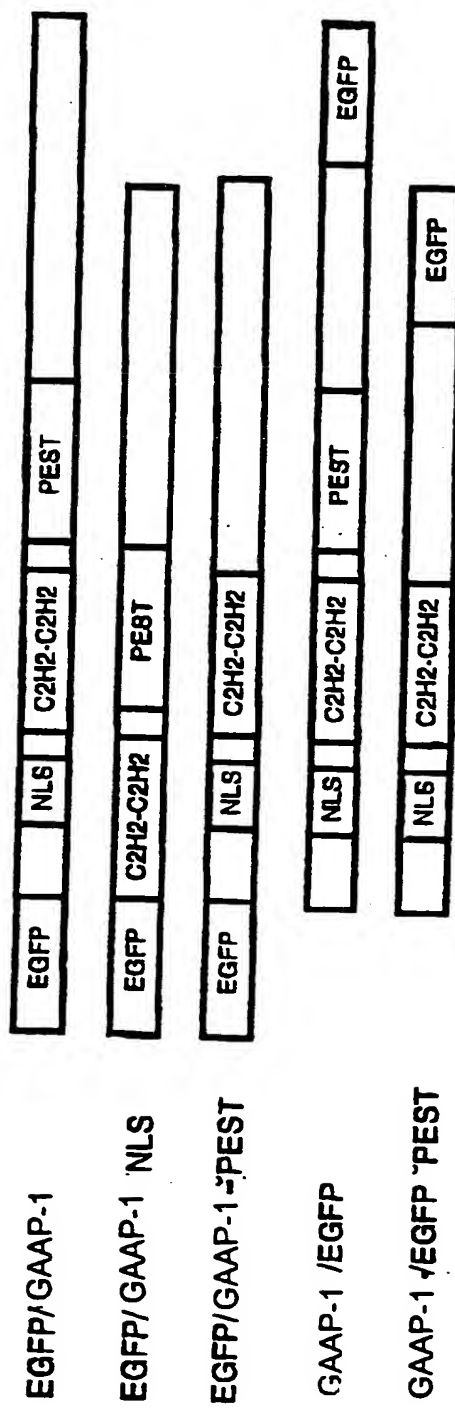
Figure 2A



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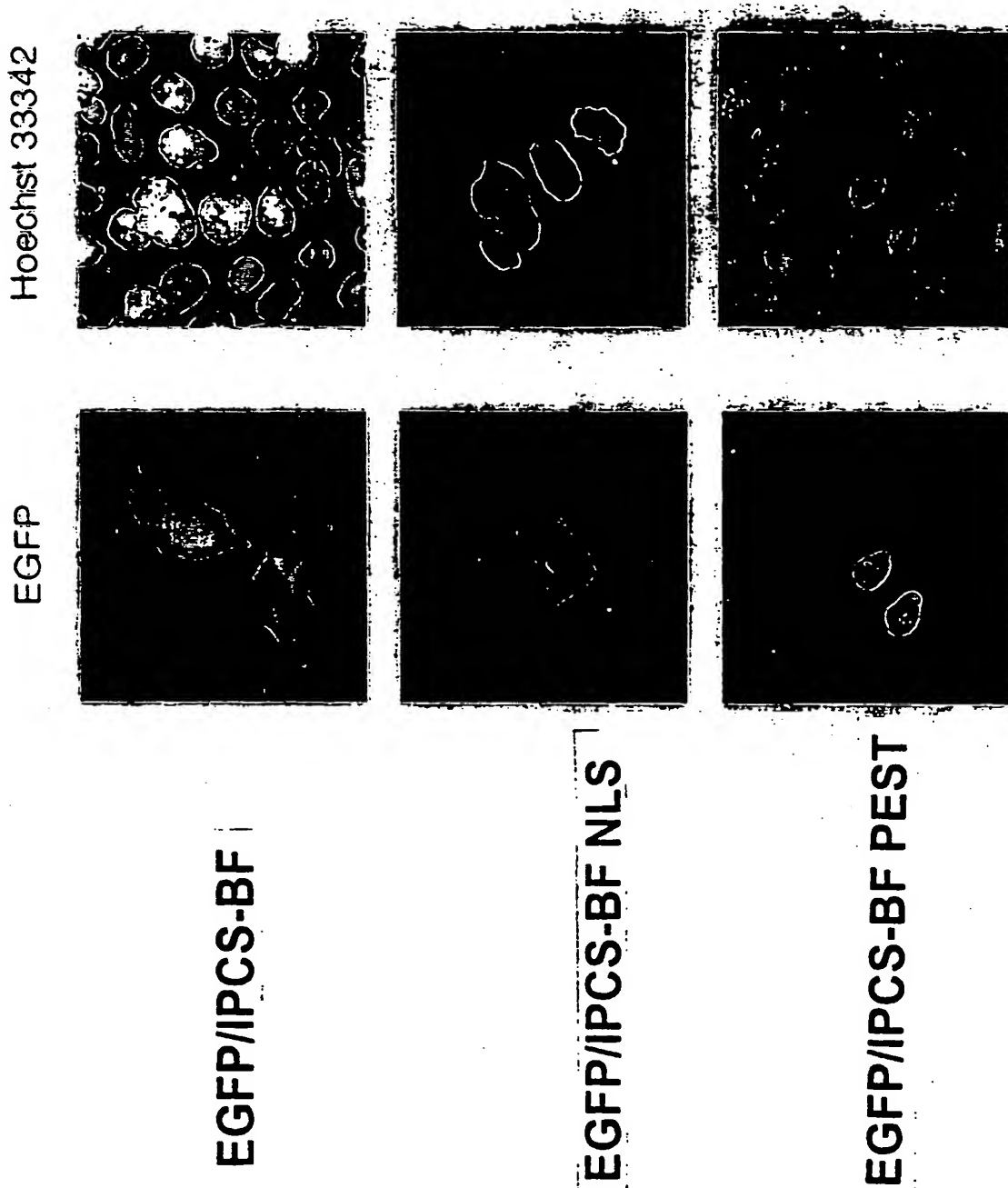
Figure 3

AA 1 M A L G N Q K S T W E F S N K D A S E I N S E Q D K E N S L I **NLS** K S E P H R I K I F
 51 D G G Y K S N E E Y V Y I R G R G R G K **CPH2** V I C E E C G I R C K K P S M I K K H I R T H T D V R P Y H
 61 I C T Y C N E S E K T K G N L T K H M K S K A H S K K C V D L G I S V G L I D E Q D T E E S D E K Q R
 151 F S Y E R S G Y D L E E S D G P D E D D N E N E D D D E D S Q A E S V L S A T P S V T A S P Q H L P
 201 S R S S L Q D P V S T D E D V R I T D C F S G V H T D P M D V L P R A L T R M T V L S T A Q S D Y
 251 N R K T L S P G K A R Q R A A R D E N D T I P S V D T S R S P C H Q M S V D Y P E S E E I L R S S M
 301 A G K A V A I T Q S P S S V R L P P A A A E H S P Q T A A G M P S V A S P H P D P Q E Q K Q Q I T L
 351 Q P T P G L P S P H T H L F S H L P L H S Q Q Q S R T P Y N M V P V G G I H V V P A G L T Y S T F V
 401 P L Q A G P V Q L T I P A V S V W H R T L G T H R N T V T E V S G T T N P A G V A E L S S V V P C I
 451 P I G Q I R V P G L Q N L S T P G L Q S L P S L S M E T V N I V G L A N T N M A P Q V H P P G L A L
 501 N A V G L Q V L T A N P S S Q S S P A P Q A H I P G L Q I L N I A L P T L I P S V S Q V A V D A Q G
 551 A P E M P A S Q S K A C E T Q P K Q T S V A S A N Q V S R T E S P Q G L P T V Q R E N A K K V L N P
 601 P A P A G D H A R L D G L S K M D T E K A A S A N H V K P K P E L T S I Q G Q P A S T S Q P L L K A
 651 H S E V F T K P S G Q Q T L S P D R Q V P R P T G L P R R Q P T V H F S D V S S D D E D R L V I A
 701 T

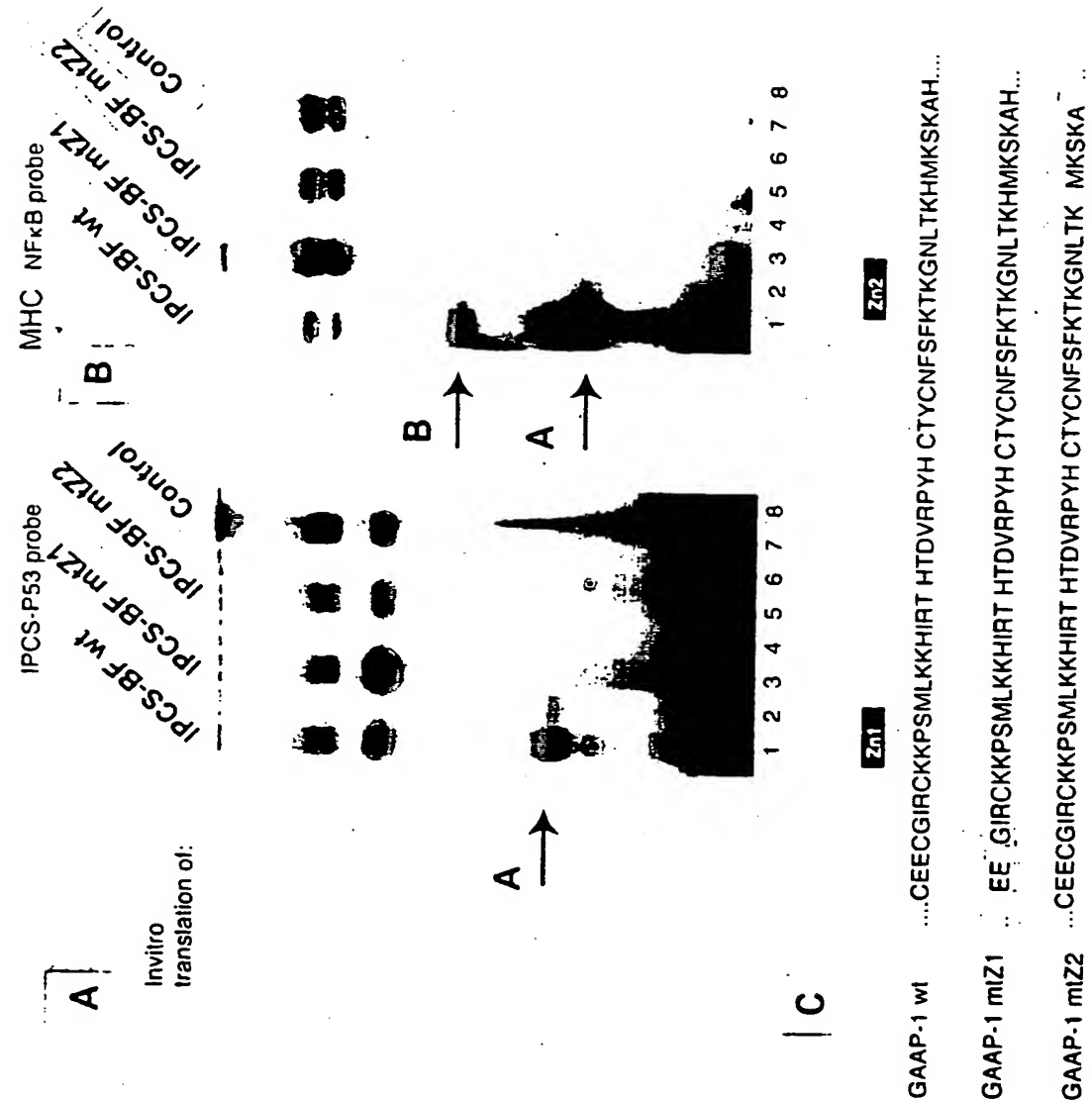
Figure 4A

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Figure 4B



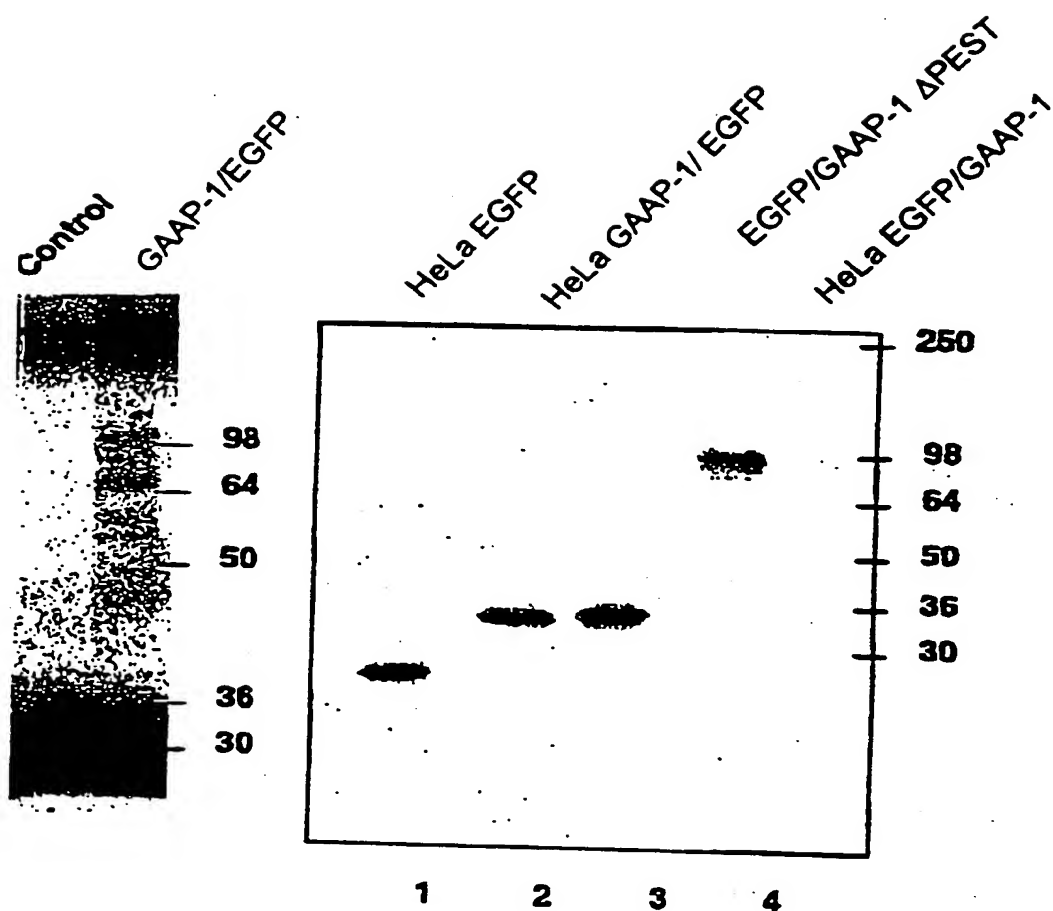
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Figure 6

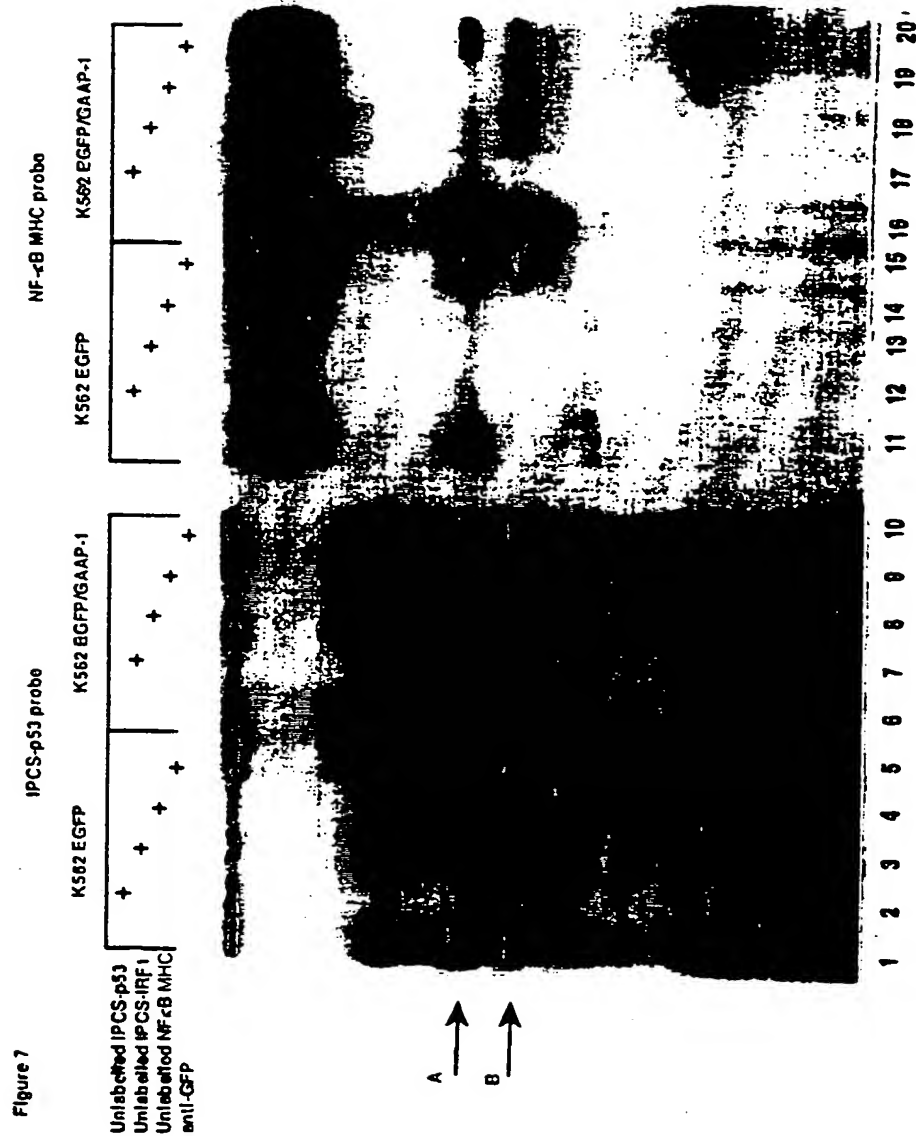


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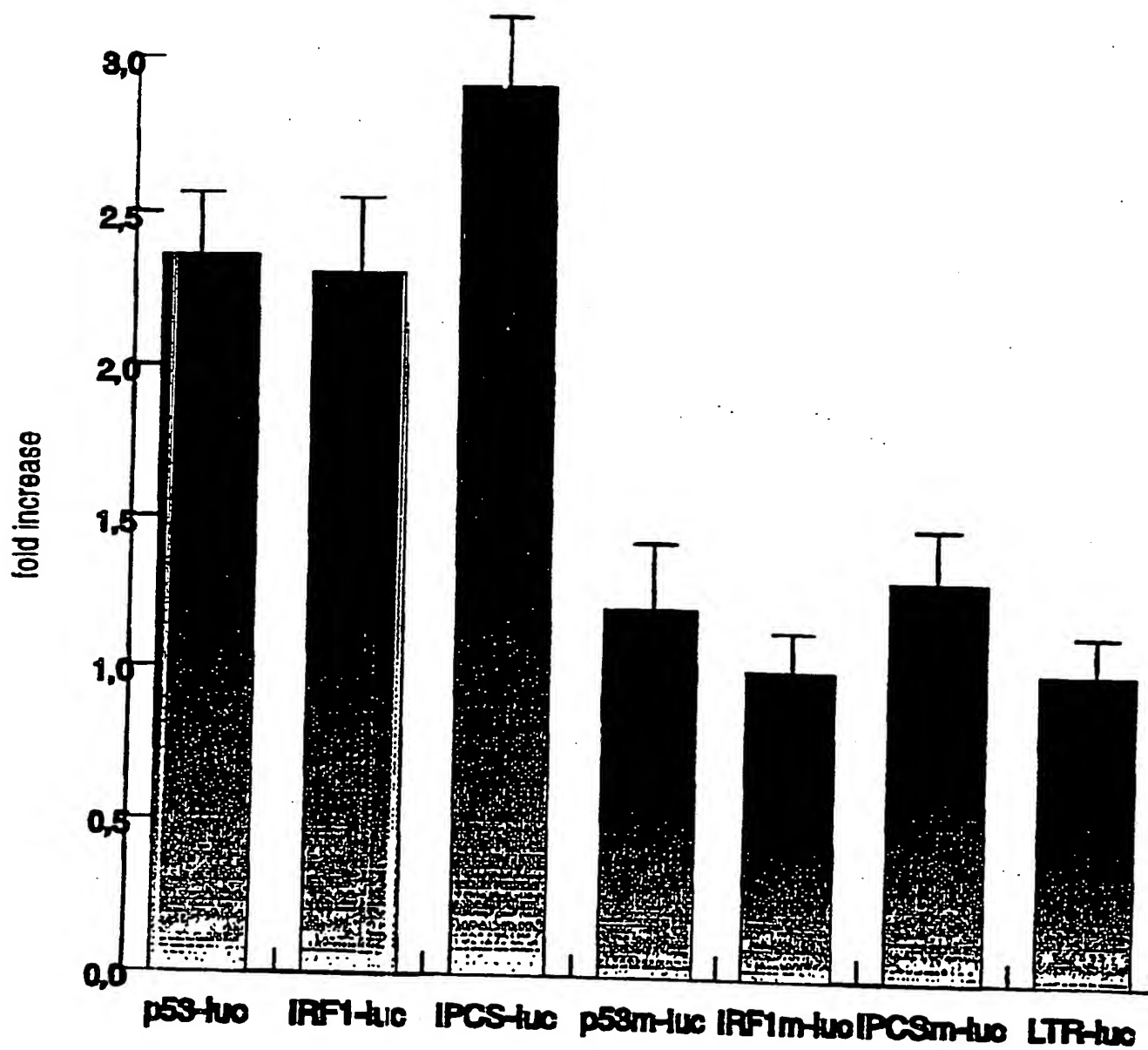
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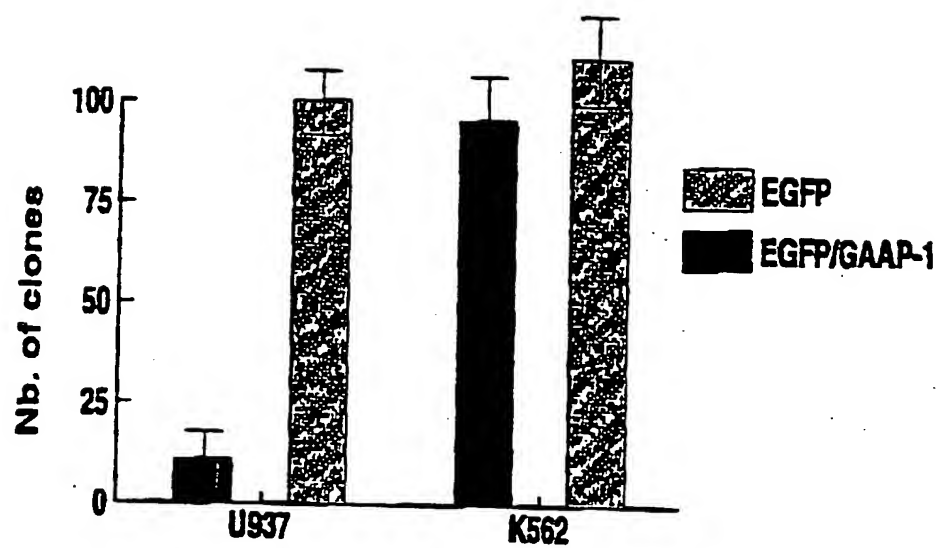
Figure 8

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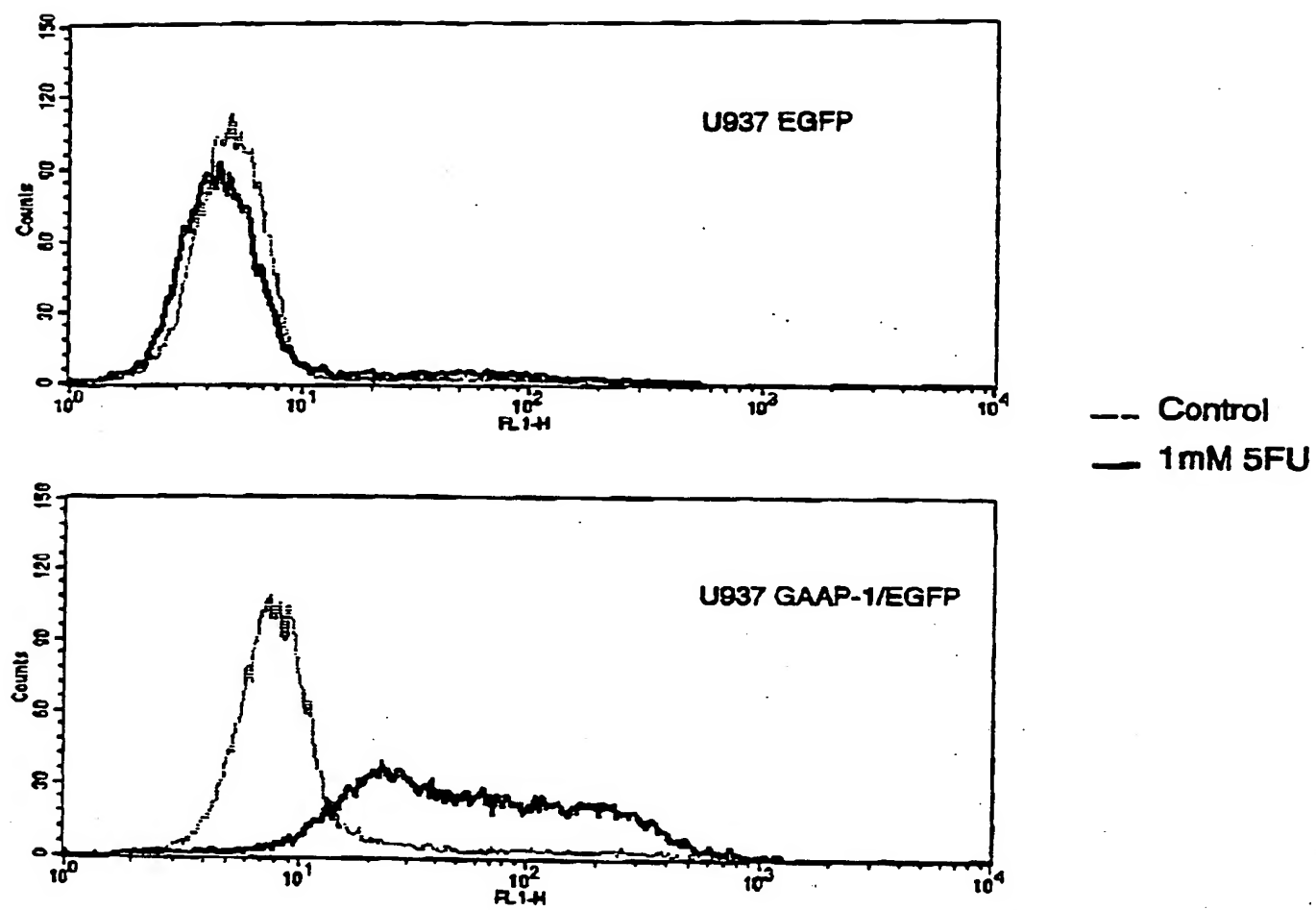
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Figure 9



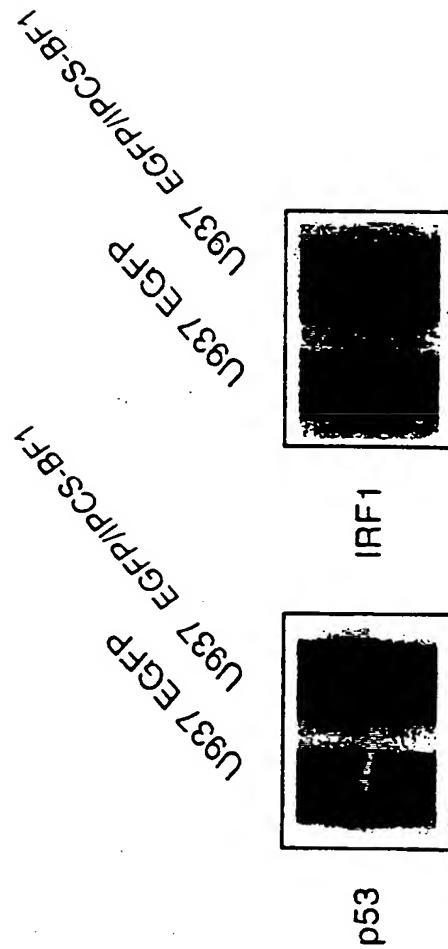
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Figure 10



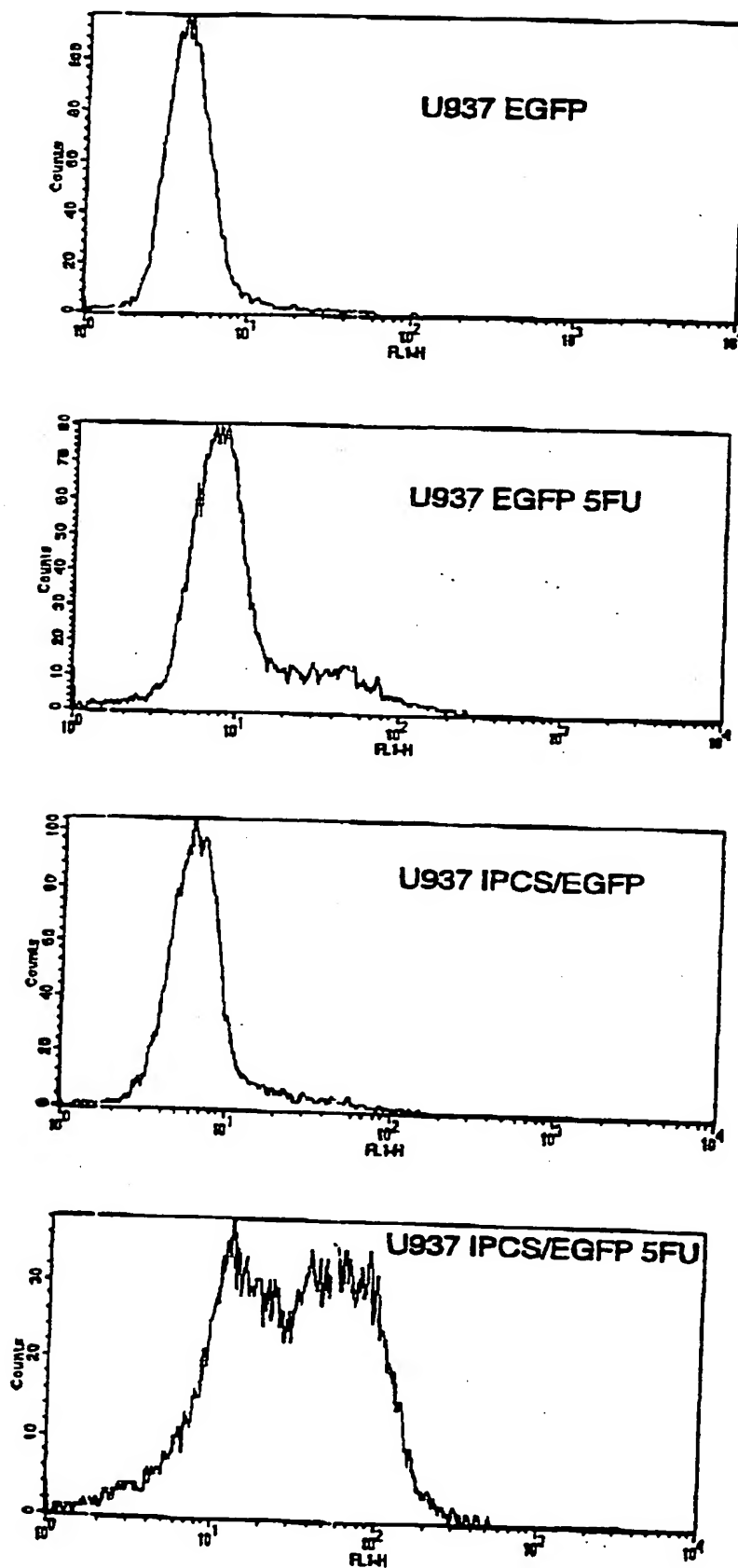
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FIGURE 11



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Figure 12



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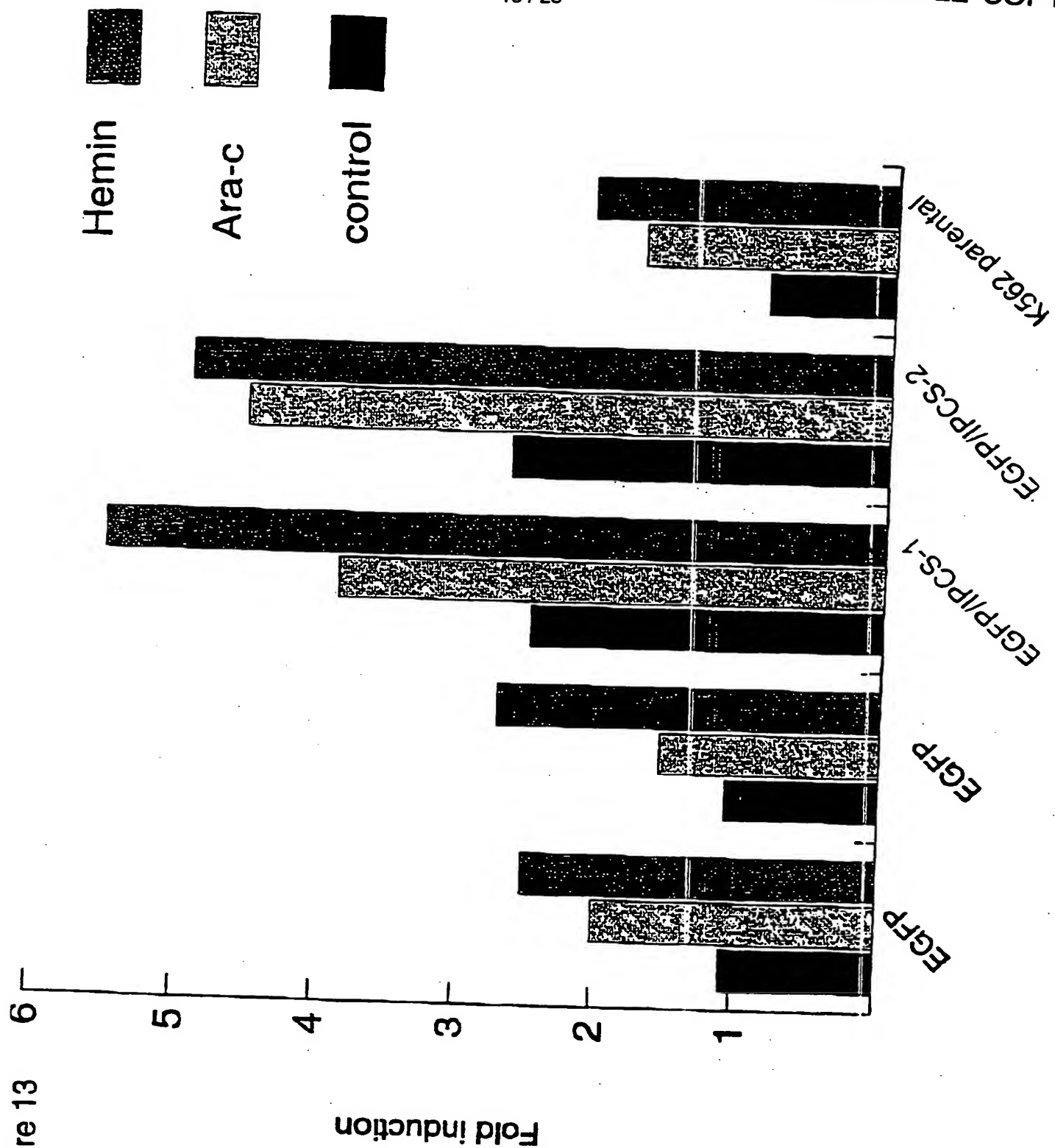


Figure 13

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1 GRP-1 CODING SEQUENCE

- Seq. No. 1

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GRP1 ATGGCATTAGGTAATCAAAAGTCCACAGTAGTTGAATTCAGCAATTAAGATGCTCTGAAATTACAGTG 70
 PRDII ATGGCATTAGGTAATCAAAAGTCCACAGTAGTTGAATTCAGCAATTAAGATGCTCTGAAATTACAGTG 70

GRP1 AGCAAGATAAGAAAATTCCTTAAATCAAAAGTGAACCAAGAGAAATTAATAATTTTGTTGGGGATATAA 140
 PRDII AGCAAGATAAGAAAATTCCTTAAATCAAAAGTGAACCAAGAGAAATTAATAATTTTGTTGGGGATATAA 140

GRP1 GTCAATCAAGAGTATGTATATGTCGGAGGCGGGGAGGAGGAATTCATTTGTGAAGAAATGTGGGAATA 210
 PRDII GTCAATCAAGAGTATGTATATATTCGGAGGCGGGGAGGAGGAATTCATTTGTGAAGAAATGTGGGAATA 210

GRP1 CGTTGTGAGAAACCTAGCCTGTGTAAGAAACACATACGAACCCCTACAGATGTGCGGCCCTACCACTGCA 280
 PRDII CGTTGTGAGAAACCTAGCCTGTGTAAGAAACACATACGAACCCCTACAGATGTGCGGCCCTACCACTGCA 280

GRP1 CTTACTGTAACTTCTCTCTTAAGACTAAAGGAATCTGACAAACACATGAGTCCAGGCCACATAGCAA 350
 PRDII CTTACTGTAACTTCTCTCTTAAGACTAAAGGAATCTGACAAACACATGAGTCCAGGCCACATAGCAA 350

GRP1 GAAATGTGTGGATTATAGCCGCTTCAGTAGGTTTAATGATCAACAGGTACAGAGAAATCAGATGAAAA 420
 PRDII GAAATGTGTGGATTATAGCCGCTTCAGTAGGTTTAATGATCAACAGGTACAGAGAAATCAGATGAAAA 420

GRP1 CAGAGATTCACTATATAGGATCTGGATATGATCTTGAGAAATCTGATGGGCCAGATGAGGATCACAAATG 490
 GRP1 CAGAGATTCACTATATAGGATCTGGATATGATCTTGAGAAATCTGATGGGCCAGATGAGGATCACAAATG 490

GRP1 AAATGTAGAGAGCTGTGAGGACAGCCAGGCTGAATCAGTCTCTGAGGACACCTTCAGTACAGCTAG 560
 PRDII AAATGTAGAGAGCTGTGAGGACAGCCAGGCTGAATCAGTCTCTGAGGACACCTTCAGTACAGCTAG 560

GRP1 CCGCAGCACTTCTCTCTAGAGTAGCTTCAGGACCTGTGAGTACTGACGAGGATGTACAGATCAC 630
 PRDII CCGCAGCACTTCTCTCTAGAGTAGCTTCAGGACCTGTGAGTACTGACGAGGATGTACAGATCAC 630

GRP1 GATTGCTTTTCTGGGGTACACAGGACCAATGGAAGCTTCTGCCCAGGGGCTCTCTACCCAGATGACTG 700
 PRDII GATTGCTTTTCTGGGGTACACAGGACCAATGGAAGCTTCTGCCCAGGGGCTCTCTACCCAGATGACTG 700

GRP1 TCTTGAGCACACACAGTCTGACTTCAATAGGAAGACACTCTCTGCGGGGAGGCCAGGCAGGGTCTGTC 770
 PRDII TCTTGAGCACACACAGTCTGACTTCAATAGGAAGACACTCTCTGCGGGGAGGCCAGGCAGGGTCTGTC 770

GRP1 GAGGATGAAAACACACAMTTCCTCTCTGAGACACTTCCAGGTCCCGGTCTCATCAGATGCTCTGTCGAC 840

FIGURE 14A (a)

PRDII GAAGATGAAGAAGACAAATTOGGTCTGTAGACACTTCCAGGTCCCGGTGTATCAGATGTCTGTGGAC 840
 GAAP1 TACCTGAGTCAGAGAAATTCAGAGAGTTCTATGGCGGAAAGCTGTCTCTTAAACACAGAGCCCAT 910
 PRDII TACCTGAGTCAGAGAAATTCAGAGAGTTCTATGGCGGAAAGCTGTCTCTTAAACACAGAGCCCAT 910
 GAAP1 CATCTGTAAAGACTTCTCTCTGTCTGCAAGCTGAGACAGCCCCAGACAGCGGGGGATGCTTCTGTGGC 980
 PRDII CATCTGTAAAGACTTCTCTCTGTCTGCAAGCTGAGACAGCCCCAGACAGCGGGGGATGCTTCTGTGGC 980
 GAAP1 CTCACACATCTCTGACCTCAAGAACAGAGCAGCAATATACCTTACAGCGGACTCCAGGCTTGGCTTCT 1050
 PRDII CTCACACATCTCTGACCTCAAGAACAGAGCAGCAATATACCTTACAGCGGACTCCAGGCTTGGCTTCT 1050
 GAAP1 CCCCACACTCATTGTGTTTGGCACTTCTCTTGGCATTOCCAGCAGCAATOGAGGACACTTATATATGG 1120
 PRDII CCCCACACTCATTGTGTTTGGCACTTCTCTTGGCATTOCCAGCAGCAATOGAGGACACTTATATATGG 1120
 GAAP1 TTCCAGTTGGGGGGATCCATGTGGTAACCTGCTGGGCTCACATACTCCAGGTTGTGGCCCCCTCAGGCTGG 1190
 PRDII TTCCAGTTGGGGGGATCCATGTGGTAACCTGCTGGGCTCACATACTCCAGGTTGTGGCCCCCTCAGGCTGG 1190
 GAAP1 ACCAGTGCAGCTCAGCATCCCTGCTGTCAGGTCTGCTTACAGAACTTTGGGTACTCATAGGATACGGTTC 1260
 PRDII ACCAGTGCAGCTCAGCATCCCTGCTGTCAGGTCTGCTTACAGAACTTTGGGTACTCATAGGATACGGTTC 1260
 GAAP1 ACAGAGGTGTCTGGCACTACAAACCTGCTGGAGTGGCTGAATTAGCAGGTGTGTGGCATGTATTCTCTA 1330
 PRDII ACAGAGGTGTCTGGCACTACAAACCTGCTGGAGTGGCTGAATTAGCAGGTGTGTGGCATGTATTCTCTA 1330
 GAAP1 TGGGCCAAATCCGGGTGGCAGGCTTCAGAACTTAGTACCCAGGCTTGCAGTCACTCCCTCTGTATAG 1400
 PRDII TGGGCCAAATCCGGGTGGCAGGCTTCAGAACTTAGTACCCAGGCTTGCAGTCACTCCCTCTGTATAG 1400
 GAAP1 CATGGAAACCGTCAATATTTGTAGGCTTAGCCATACAAATATGGCCCCCAAGTCCATCCACAGGACTG 1470
 PRDII CATGGAAACCGTCAATATTTGTAGGCTTAGCCATACAAATATGGCCCCCAAGTCCATCCACAGGACTG 1470
 GAAP1 GCTCTGTGATGCTGTGGACTCCAGGTTCTGACTGCAAAACCTTCACTACAAAGCAGCCCCCGCCCTCAGG 1540
 PRDII GCTCTGTGATGCTGTGGACTCCAGGTTCTGACTGCAAAACCTTCACTACAAAGCAGCCCCCGCCCTCAGG 1540
 GAAP1 CACACATTCCAGGTCTCCAGATCTTGAACATAGCAATTGCCAAGTTAATCCCTCAGTCAGTCAAGTGGC 1610
 PRDII CACACATTCCAGGTCTCCAGATCTTGAACATAGCAATTGCCAAGTTAATCCCTCAGTCAGTCAAGTGGC 1610
 GAAP1 CGTGTGTGCACAGGAGCTCCGCAATGCCAGCTTCCCAAGCAAGCATGGGAGACACAAACCAAGCAG 1680

FIGURE 14A (b)

PRDII CGTTGATGCACAGGGAGCTCCAGAAATGCCAGCTTCCCAAGCAAGCATGCCGACACAAACCCAGCAG 1680
 GRAP1 ACTTCTGTAGCCAGGGCAAAACCAGGTACGCAAGCACTAGTCTCTCAGGGGTTACCTACAGTCCAGGGG 1750
 PRDII ACTTCTGTAGCCAGGGCAAAACCAGGTACGCAAGCACTAGTCTCTCAGGGGTTACCTACAGTCCAGGGG 1750
 GRAP1 AAAATGCCAAAAAGTTCTGAATCCACTGCCCCCTGCAGGTGACCATGCCAAGGCTTGATGGGCTGAGTAA 1820
 PRDII AAAATGCCAAAAAGTTCTGAATCCACTGCCCCCTGCAGGTGACCATGCCAAGGCTTGATGGGCTGAGTAA 1820
 GRAP1 AATGGACACACAGAGAGGCTGGCTGGGCAATCAGGTGAGGCCCCAAGGCTGACTCACTTCCATACAGGGC 1890
 PRDII AATGGACACACAGAGAGGCTGGCTGGGCAATCAGGTGAGGCCCCAAGGCTGACTCACTTCCATACAGGGC 1890
 GRAP1 CAACCAGGGTCCAGGTACAAACCTCTGCTGAGGCCACTTCTGAGTTTTCACAAAGGCCCTCAGGGCCAGC 1960
 PRDII CAACCAGGGTCCAGGTACAAACCTCTGCTGAGGCCACTTCTGAGTTTTCACAAAGGCCCTCAGGGCCAGC 1960
 GRAP1 AGACTCTCTCTCCAGACAGACAGGTTCAGGGCCACAGCACTACCCGGGAGGCGAGGCCACTGTGCACCT 2030
 PRDII AGACTCTCTCTCCAGACAGACAGGTTCAGGGCCACAGCACTACCCGGGAGGCGAGGCCACTGTGCACCT 2030
 GRAP1 CAGCGAGGTGAGCAGCGATGCTGACGAGGACAGGCTTGATGATGCCAACTGATG 2084
 PRDII CAGCGAGGTGAGCAGCGATGCTGACGAGGACAGGCTTGATGATGCCAACTGATG 2084

FIGURE 14A (c)

ATGGGGCAGAAGTTTCAAAAAAAGAGA

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GCATTAGGTAATCAAAGTCCACAGTACGTTGAATTCAGCAATTAAGGTGCTCTCGAATTACAGTG

GAAP1 AGCAAGATAAAGAAATTCCTTAATCAAAGTGAACCCAGAGATTAAATATTTCATGGAGGTATTA

GAAP1 GTCAATCAAGAGTATGTATATGTCCGAGGCACCCAGAGGGAATACATTTCGAGAGATGTCGAATA

GAAP1 CGTTGTAAAGAACTTACATGTTAAAGAAACACTAGCAACCCATACAGATGTCCGCCCCCAACACTGCA

GAAP1 CTACTGTACTTCTCTCTTAAGCTAAAGGAATCTGACAAACACATGAAGTCCAGGCACATAGCAA

GAAP1 GAATGTGAGGCAATTAGGCGTCTCAGTAGGTTAATGATCAACAGGTACAGAGATCAGATGAAAAA

GAAP1 CAGCAATCAGTTATGAGCATCTCGATATGCTTGAACATCTGATGGCCAGATCAGGATCACAATG

GAAP1 AAATGTAGAGCATGATGAGGACAGCCAGGCTGAATCAGTCTCTCAGCCACCCCTAGTACAGCTAG

GAAP1 CCGGCAGCACTTCCATCTAGAGTAGCCTCAGGACCCCTGTAGTACTGACAGGATGTCAAGGTCAAC

GAAP1 GATTGCTTTTCTGGGCTACACAGGACCCATGTGCTTCTGCCCAGGCGCTCTCAACCAATGACTG

GAAP1 TCTGTAGCACAGGCAGTCTGACTACATAGGAGCACTCTCTCCGGGCTAGCCACCCAGGCTGCTGC

GAAP1 GACAGATCAAAACACCAATTCGTTCTGTAGCACTTCCAGGTCCCGGTGTCATCAATGCTCTGTGCAC

FIGURE 14B (a)

GAAP1 TACCTGAGTCAGAGAAATTCAGAGAGTTCTATGGCAGGAAAGCTGTTCCTATACACAGAGGCGAT

GAAP1 CATCTGTAAAGACTTCCTCTCTGCTGACGCTGAGCACAGGCGGACAGAGCGGGGGATGCGTTCTGTGGC

GAAP1 CTCACCATCTCTGACCTTCAGTACAGTACGAGCAATTAATCTCTACAGGCGCTCAGGCTTGCGTTCT

GAAP1 CCGCACACTCATTTGTTTACGACCTTCCTTTGCAATTCAGCAGCAATCGAGGACACCTTATATATATGG

GAAP1 TTCCAGTGGGGGGATCCATGTGGTAAGTCTGCTGGGCTCACATACTCCAGCTTTGTGGGCGTTCAGGCTGG

GAAP1 ACCAGTGCAGCTCAGATTCCTCTGCTGCTAGTGTCTGTACAGTACTTTGGGTACTCATAGCAATACGGTC

GAAP1 ACAGAGTGTCTGGCACTACAAACCTGCTGGAGTGGCTGAATTAAGCAGTGTCTGCGCATGTATTCCTA

GAAP1 TGGGCAATTCGGGTGGCAGGCGTTCAGAACCTAAGTACCGCAGGCTTGCACTCAGTCCGCTGTGTTAAG

GAAP1 CATGGAAACGTCATATTTGTAGGCTTACCAATACAAATATGGCGGACAGTCCATCCACAGGACTG

GAAP1 GCTCTGAATGCTGTGGGACTCCAGGTTCTGACTGCAAAACCTTCATCAAAAGCAGCGCGCGCGCTCAGG

GAAP1 CACACATTCAGGTTCTCCAGTCTTTGACATAGCAATGGGCACTTAATCCGCTCAGTCAAGTACAGC

GAAP1 CGTTGATCCACAGGAGCTCGGCAATGGCAGCTTCGCAAGCAAGCATGGTAGCACAAACCTACGAG

FIGURE 14B (b)

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PRDII CGTTCATGCACAGGGAGCTCCAGAAATGCGAGCTTCCAAAGCAAGCATGCGACATCAACCCAGCAG

GAAP1 ACTTCTGTAGCCAGGGCAAAACAGGTACGACGGAACCGTCTCTCTCAGGGGTACCTACAGTCCAGGGG

GAAP1 AAAATGCAAAAAAGCTTCTGAATCCACCTGCCCCCTCCAGGTGACCATGCAAGGCTTGATGGCTGAGTAA

GAAP1 AATGGACACAGAGAGGCTGCGCTGGGCAAAATCAGGTGAAGGCCAAGCTGAACTCACTTCCATACAGGGC

GAAP1 CAACAGGGTCCAGGTACAAACCTCTGCTGAAGGCACATTCTGAAGTTTTACAAAGGCCCTCAGGCCAGC

GAAP1 AGACTCTCTCTCCAGACAGACAGGTTCGCCAGGCCACAGCACTACGGGGAGGCCAGGCCACTGTGCACIT

GAAP1 CAGCGAGGTGAGCAGGATGATGAGGAGGACAGGCTTGTGATAGCAACCTGATG

FIGURE 14B (c)

GAAP-2 coding seq

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Seq No. 5

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1  ATGGGGCAGA AGTTTCAAAA AAAGAAATCT TACAGGCTGG TGTTAAAGGA
   TACCCCGTCT TCAAAGTTTT TTTCTTTAGA ATGTCCGACC ACAATTTCTT
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51  ACTTCGGAAT CCCTTAAAGA GAGCATTAGG TAATCAAAG TCCACAGTAG
   TGAAGCCTTA GGAATTTCT CTCGTAATCC ATTAGTTTTT AGGTGTCATC
-----
101 TTGAATTCAG CAATAAGAT GCCTCTGAAA TTAACAGTGA GCAAGATAAA
   AACTTAAGTC GTTATTTCTA CGGAGACTTT AATTGTCACT CGTTCATTT
-----
151 GAAAATTCCT TAATCAAAG TGAACCAAGA AGAATTAAJA TATTTGATGG
   CTTTTAAGGA ATTAGTTTTT ACTTGGTTCT TCTTAATTTT ATAACTACC
-----
201 AGGATATAAG TCAATGAAG AGTATGTATA TATCCGAGGC AGGGGAAGAG
   TCCTATATTC AGTTTACTTC TCATACATAT ATAGGCTCCG TCCCTTCTC
-----
251 GAAAATACAT TTGTGAAGAA TGTGGAATAC GTTGTAAAGAA ACCTAGCATG
   CTTTATGTA AACACTTCTT ACACCTTATG CAACATTCCT TGGATCGTAC
-----
301 TTAAGAAAC ACATACGAAC CCATACAGAT GTCCGCCCCC ACCACTGCAC
   AATTTCTTTG TGTATGCTTG GGTATGTCTA CAGGCGGGGA TGGTGACGTG
-----
351 TTAAGTAAC TTCTCCTTTA AGACTAAAGG AAATCTGACA AAACACATGA
   AATGACATTG AAGAGGAAAT TCTGATTTCC TTTAGACTGT TTTGTGTACT
-----
401 AGTCCAAGGC ACATAGCAAG AAATGTGTGG ATTTAGGCAT CTCAGTAGGT
   TCAGGTTCCG TGTATCGTTC TTTACACACC TAAATCCGTA GAGTCATCCA
-----
451 TTAATAGATG AACAGGATAC AGAAGAATCA GATGAAAAAC AGAGATTGAG
   AATTATCTAC TTGTCTATG TCTTCTTAGT CTACTTTTIG TCTCTAAGTC
-----
501 TTATGAGCGA TCTGGATATG ATCTTGAAGA ATCTGATGCC CCAGATGAGG
   AATACTCGCT AGACCTATAC TAGAATTCT TAGACTACCG GGTCTACTCC
-----
551 ATGACAATGA AAATGAAGAC GATGATGAGG ACAGCCAGGC TGAATCAGTC
   TACTGTTACT TTTACTTCTG CTACTACTCC TGTCGGTCCG ACTTAGTCAG
-----
601 CTGTCAGCCA CACCCTCAGT CACAGCTAGC CCGCAGCACC TTCCATCTAG
   GACAGTCGGT GTGGGAGTCA GTGTCGATCG GGCCTCGTGG AAGGTAGATC
-----
651 AAGTAGCCTT CAGGACCTTG TGAGTACTGA CGAGGATGTC AGGATCACCG
   TTCATCGGAA GTCCTGGGAC ACTCATGACT GCTCCTACAG TCCTAGTGSC
-----
701 ATTGCTTTTC TGGGGTACAC ACGGACCCAA TGGACGTTCT GCCCAGGGCG
   TAACGAAAG ACCCATGTG TGCTTGGGTT ACCTGCAAGA CGGGTCCCGC
-----
751 CTGCTCACC AATGACTGT CCTGAGCACA GCACAGTCTG ACTACAATAG
   GACGATGGT CTTACTGACA GGACTCGTGT CGTGTGAGC TGATGTTATC
-----
801 GAAGACACTC TCTCCGGGGA AGGCCAGGCA GCGTGCTGCS AGAGATGAAA
   CTTCTGTGAG AGAGGCCCCC TCCGGTCCGT CGCAGGACG TCTTACTTT
-----
851 ACGACACAAT TCCGTCTGTA GACACTTCCA GGTCCCCGTG TCATCAGATG
   TGCTGTGTTA AGGCAGACAT CTGTGAAGGT CCAGGGGCA AGTAGTCTAC
-----
901 TCTGTGGACT ACCCTGAGTC AGAAGAAATT CTGAGAAGTT CTATGGCAGG
   AGACACCTGA TGGGACTCAG TCTTCTTTAA GACTTTCA GATACCGTCC
-----

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FIGURE 14C (a)

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951  AAAAGCTGTT GCTATAACAC AGAGCCCATC ATCTGTAAGA CTCCTCCTG
      TTTTCGACAA CGATATTGTG TCTCGGGTAG TAGACATTCT GAAGGAGGAC
-----
1001  CTGCAGCTGA GCACAGCCCC CAGACAGCAG CGGGGATGCC TTCTGTGGCC
      GACCTCGACT CGTGTCTGGG GTCTGTCTGC GCCCTTACCG AAGACACCGG
-----
1051  TCACCACATC CTGACCCTCA AGAACAGAAG CAGCAAATTA CTCTACAGCC
      AGTGGTGTAG GACTGGGAGT TCTTGTCTTC GTCGTTTATT GAGATGTCGG
-----
1101  GACTCCAGGC TTGCCTTCTC CCCACACTCA TTTGTTTAGC CACCTTCCTT
      CTGAGGTCCG AACGGAAGAG GGGTGTGAGT AAACAAATCG GTGGAAGGAA
-----
1151  TGCATTCCCA GCAGCAATCG AGGACACCTT ATAATATGCT TCCAGTTGGG
      ACGTAAGGGT CGTCGTTAGC TCCTGTGGAA TATTATACCA AGGTCAACCC
-----
1201  GGGATCCATG TGGTACCTGC TGGCCTCACA TACTCCACGT TTGTGCCCTT
      CCCTAGGTAC ACCATGGACG ACCGGAGTGT ATGAGGTGCA AACACGGGGA
-----
1251  TCAGGCTGGA CCAGTGCAGC TCACGATCCC TGCTGTCACT GTCGTTTACA
      AGTCCGACCT GGTACGTCG AGTGCTAGGG ACGACAGTCA CAGCAAGTGT
-----
1301  GAACCTTGGG TACTCATAGG AATACGGTCA CAGAAGTGTG TGGCACTACA
      CTTGAAACCC ATGAGTATCC TTATGCCAGT GTCTTCACAG ACCGTGATGT
-----
1351  AACCCTGCTG GAGTGGCTGA ATTAAGCAGT GTTGTGCCAT GTATTCTAT
      TTGGGACGAC CTCACCGACT TAATTCGTCA CAACACGGTA CATAAGGATA
-----
1401  CGGCCAAATC CGCGTGCCAG GCCTTCAGAA CCTAAGTACT CCAGGCTTGC
      GCCGGTTTAG GCGCACGGTC CGGAAGTCTT GGATTTCATG GGTCCGAACG
-----
1451  AGTCACTCCC CTCGTTAAGC ATGGAAACCG TCAATATTGT AGGCCTAGCC
      TCAGTGAGGG GAGCAATTCT TACCTTTGGC AGTTATAACA TCCGGATCGG
-----
1501  AATACAAATA TGGCCCCACA AGTCCATCCA CCAGGACTGS CTCTGAATGC
      TTATGTTTAT ACCGGGGTGT TCAGGTAGGT GGTCTGTAGC GAGACTTACG
-----
1551  TGTCGGACTG CAGGTTCTGA CTGCAAACCC TTCATCACA AGCAGCCCCG
      ACAGCCTGAC GTCCAAGACT GACGTTTGGG AACTAGTGT TCGTCGGGGC
-----
1601  CCCCTCAGGC ACACATTCCA GGTCTCCAGA TCTTGAACA AGCATTGCCC
      GGGGAGTCCG TGTGTAAGGT CCAGAGGTCT AGAACTTGTA TCGTAACGGG
-----
1651  ACCTTAATCC CCTCAGTCAG TCAAGTAGCC GTTGATGCAC AGGGAGCTCC
      TGGAAATTAGG GGAGTCAGTC AGTTCATCGG CAACTACGTG TCCCTCGAGG
-----
1701  AGAAATGCCA GCTTCCCAA GCAAAGCATG CGAGACACA CCCAAGCAGA
      TCTTTACGGT CGAAGGGTTT CGTTTCGTAC GCTCTGTGTT GGGTTCGTCT
-----
1751  CTTCTGTAGC CAGCGCAAAC CAGGTCAGCA GGACCGAGTC TCCTCAGGGG
      GAAGACATCG GTCGCGTTTG GTCCAGTCGT CCTGGCTCAG AGGAGTCCCC
-----
1801  TTACCTACAG TCCAGCGGGA AAATGCAAAA AAGTTCTGA ATCCACCTGC
      AATGGAATGC AGGTGCGCCCT TTTACGTTTT TTTCAAGAC TAGGTGGACC
-----
1851  CCCTGCAGGT GACCATGCAA GGCTTGATGG CCTGAGTAA ATGGACACAG
      GGGACGTCCA CTGGTACGTT CCGAACTACC GGACTCATT TACCTGTGTC
-----

```

FIGURE 14C (b)

1901 AGAAGGCTGC CTCGGCAAAT CACGTGAAGC CCAAGCCTGA ACTCACTTCC
TCTTCCGACG GAGCCGTTTA GTGCACITCG GGTTCGGACT TGAGTGAAGG

1951 ATACAGGGCC AACCAGCGTC CACGTCACAA CCTCTGCTGA AGGCACATTC
TATGTCCCGG TTGGTCGCAG GTGCAGTGTG GGAGACGACT TCCGTGTAAG

2001 TGAAGTTTTT ACAAAGCCCT CAGGCCAGCA GACTCTCTCT CCAGACAGAC
ACTTCAAAAA TGTTTCGGGA GTCCGGTCGT CTGAGAGAGA GGTCTGTCTG

2051 AGGTTCCCGG GCCCACAGGA CTACCGCGGA GGCAGCCCAC TGTGCACTTC
TCCAAGGGTC CGGGTGTCTT GATGGCGCCT CCGTCGGGTG ACACGTGAAG

2101 AGCGACGTGA GCAGCGATGA TGACGAGGAC AGGCTTGTGA TAGCAACCTG
TCGCTGCACT CGTCGCTACT ACTGCTCCTG TCCGAACAAT ATCGTTGGAC

2151 A
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FIGURE 14C (c)

2 GAAP-1 POLYPEPTIDE

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*GAAP-1	
GAAP1	MALGNQKSTWVEFSNKRASEINSEQKRENSLRSEPRKRIKFDGGYKNEBYVYVRGCGGKYTCRECGI 70
PRDII	MALGNQKSTWVEFSNKRASEINSEQKRENSLRSEPRKRIKFDGGYKNEBYVYVRGCGGKYTCRECGI 70
GAAP1	RCKGPSMLKKHHRHIDVRPYHCTYCNFSPTKRGMLTKHMSKAHKKCVILGWSVGLIDEQDTRSDK 140
PRDII	RCKGPSMLKKHHRHIDVRPYHCTYCNFSPTKRGMLTKHMSKAHKKCVILGWSVGLIDEQDTRSDK 140
GAAP1	QRFPSYERSGYDLSESDGPFDDNENEDDDDSQAESVLSTPSVITASPOHLPSRSSLQDPVSTDEIVRTT 210
PRDII	QRFPSYERSGYDLSESDGPFDDNENEDDDDSQAESVLSTPSVITASPOHLPSRSSLQDPVSTDEIVRTT 210
GAAP1	DCFSGVHTDPMVLPRALLTRMTVLSTAQSDYNRKLSFGARQRAARDENDITPSVDTSRSPCHQMSVD 280
PRDII	DCFSGVHTDPMVLPRALLTRMTVLSTAQSDYNRKLSFGARQRAARDENDITPSVDTSRSPCHQMSVD 280
GAAP1	YFSEETLRSSMAGKAVATTQSPSSVRLPFAAAEHSPTAAGMPSVASPHFDQEQKQQTILQPTFGLPS 350
PRDII	YFSEETLRSSMAGKAVATTQSPSSVRLPFAAAEHSPTAAGMPSVASPHFDQEQKQQTILQPTFGLPS 350
GAAP1	PETHLFSHLPILHSQQQSETPFAMVPVGGIRWVPAGLITYSTFVPLQAGFVQLITPAVSWBERTLGTHRTIV 420
PRDII	PETHLFSHLPILHSQQQSETPFAMVPVGGIRWVPAGLITYSTFVPLQAGFVQLITPAVSWBERTLGTHRTIV 420
GAAP1	TEVSGTINEAGVAELSSWFCEIPIGQIRVPGQLNLSTFGLOSLPGLSMETATVGLANDMAFQVHPFGL 490
PRDII	TEVSGTINEAGVAELSSWFCEIPIGQIRVPGQLNLSTFGLOSLPGLSMETATVGLANDMAFQVHPFGL 490
GAAP1	ALNAVGLQVLITANPSSQSSPAPQAHIPGLQILNIALPTILPSVSQVAVDQCAPMEASQSKACETQPRQ 560
PRDII	ALNAVGLQVLITANPSSQSSPAPQAHIPGLQILNIALPTILPSVSQVAVDQCAPMEASQSKACETQPRQ 560
GAAP1	TSVASANQVSRITESPQGLPTVQRENARKVLNPPAPAGDHARLDGLSRMDTERAASANEVKKPELITSIQ 630
PRDII	TSVASANQVSRITESPQGLPTVQRENARKVLNPPAPAGDHARLDGLSRMDTERAASANEVKKPELITSIQ 630
GAAP1	QFASTSQPLLKAHSEVFTKPSGQQTLSFDRQVFRPTALERRQPTVHFSDVSSDDDEORLWTAT 694
PRDII	QFASTSQPLLKAHSEVFTKPSGQQTLSFDRQVFRPTGLERRQPTVHFSDVSSDDDEORLWTAT 694

FIGURE 15 A

2 GAAP-1 POLYPEPTIDE

Seq No 4

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>GAAP-1

M GQKFQKKR . ALGQKSTWVEFSNRDASEINS EDDKENS LIRSEPRRIKIPDGYSNEEVVYVRGSGGKYICEBOGI

GAAP1 RCKGPSMLRKHIRKHTOVRPYHCTYCNFSPTKGNLTRHMRSGHRRKCVILGVSUGLIDSQOTEESEDEK

GAAP1 QRFYSYERSGYDLESQDGFDEDDNENEDDDSDQAESVLSATPSVITASPQHLPSSSLQDPVSTDEVRIT

GAAP1 DCFSGVEIDEMDVLPRALLTRMTVLSTAQSDYNRRILSPGRARQRAARDENDITFSVDTSRSPCHQMSVD

GAAP1 YPESSEILRSSMAGKAVAITQSPSSVRLPFAAAEHSPTAAGNPSVASPHDPQEQEQOITLOPTGLPS

GAAP1 PHIRLFSHLPFHSQQSPTPYNMVPGGIRWVPAGLTYSTFVLOAGPVQITFAVSVWHRTLGTHRTV

GAAP1 TEVSGTINPAGVAELSSWPCITGQIRVPGLQNLSTFGLQSLPSLSMEIVNIVGLANDMAPQVHPGL

GAAP1 AANAUGLQULTANPSSQSSPAPQAHIFGLQILNIALFILIPSVSQVAVDAGAPEMPASQSGACETOPRO

GAAP1 TSVASANQVERTESQGLPTVQRENARKVLNPPAPAGCHARLDGLSKMUTEKAASANEVKKPELTSIQG

GAAP1 QPASTSQPLLKAHSEVFTFSGQQLSPDRQVFRPTALRRQPTVHFSQVSSDDDEDLVIAT

FIGURE 15 B

GAAP-2 - Seq No. 6.

1 MGQKFQKKKS YRLVLKELRN PLKRALGNQK STVVEFSNKD ASEINSEQDK

51 ENSLIKSEPR RIKIFDGGYK SNEEYVYIRG RGRGKYICEE CGIRCKKPSM

101 LKKHIRTHTD VRPYHCTYCN FSFKTKGNLT KPMKSKAHSK KCVDLGISVG

151 LIDEQDTEES DEKQRFYSYER SGYDLEESDG PDEDDNENDO DDEDSQAESV

201 LSATPSVTAS PQHLPSRSSL QDPVSTDEDV RITDCFSGVH TDFMDVLPRA

251 LLTRMTVLST AQSDYNRCTL SPGKARQRAA RDENDTIPSV DTSRSPCHQM

301 SVDYPESEEI LRSSMAGKAV AITQSPSSVR LPPAAAEHSP QTAAGMPSPA

351 SPHPDPQEQK QQITLQPTPG LPSPHTHLFS HLPPLHSQQQS RTPYNMVPVG

401 GIHVVPAGLT YSTFVPLQAG PVQLTIPAVS VVHRTLGTNR NTVTEVSGTT

451 NPAGVAELSS VVFCIPIGQI RVPGLQNLST PGLQSLPSLS METVNIVGLA

501 NTNMAPOVHP PGLALNAVGL QVLTANPSSQ SSPAPQAHIP GLOILNIALP

551 TLIPSVSQVA VDAQGAPEMP ASQSKACETQ PKQTSVASAN QVSRTEPQG

601 LPTVQRENAK KVLNPPAPAG DHARLDGLSK MDTEKAASAN HVKPKPELTS

651 IQGQPASTSQ PLLKAHSEVF TKPSGQOTLS PDRQVPRPTG LPRRQPTVHF

701 SDVSSDDDED RLVIAT

FIGURE 15 C

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Figure 16

